

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/565,020  
Source: IFUJP  
Date Processed by STIC: 1-27-06

***ENTERED***



IFWP

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/565,020

DATE: 01/27/2006

TIME: 10:01:12

Input Set : F:\PR60235USw SEQ LIST.txt  
Output Set: N:\CRF4\01272006\J565020.raw

```

4 <110> APPLICANT: SmithKline Beecham Corporation
5 Lambert, Millard H
6 Xu, Robert
7 Wisely, Bruce
8 Collins, Jon
10 <120> TITLE OF INVENTION: CAR LIGAND-BINDING DOMAIN POLYPEPTIDE CO-CRYSTALLIZED WITH A
11 LIGAND, AND METHODS OF DESIGNING LIGANDS THAT MODULATE CAR
12 ACTIVITY
14 <130> FILE REFERENCE: PR60235
C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/565,020
C--> 16 <141> CURRENT FILING DATE: 2006-01-18
16 <150> PRIOR APPLICATION NUMBER: 60/488,415
17 <151> PRIOR FILING DATE: 2003-07-18
19 <160> NUMBER OF SEQ ID NOS: 7
21 <170> SOFTWARE: PatentIn version 3.2
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1450
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (273)..(1316)
32 <400> SEQUENCE: 1
33 gtgagcttc tccttaagtt acaggaactc tccttataat agacacttca ttttcctagt 60
35 ccatccctca tgaaaaatga ctgaccactg ctgggcagca ggagggatga taatcctaac 120
37 tccaaatcact gcacttctt gagatcagag gaaaaccagg aacagcgtgg gagtttgggg 180
39 agaggcattc cataccagat tctgtggct gcaggtgaca tgctgcctaa gagaagcagg 240
41 agtctgtgac agccacccca acacgtgacg tc atg gcc agt agg gaa gat gag 293
42 Met Ala Ser Arg Glu Asp Glu
43 1 5
45 ctg agg aac tgt gtg gta tgt ggg gac caa gcc aca ggc tac cac ttt 341
46 Leu Arg Asn Cys Val Val Cys Gly Asp Gln Ala Thr Gly Tyr His Phe
47 10 15 20
49 aat gcg ctg act tgt gag ggc tgc aag ggt ttc ttc agg aga aca gtc 389
50 Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Val
51 25 30 35
53 agc aaa agc att ggt ccc acc tgc ccc ttt gct gga agc tgt gaa gtc 437
54 Ser Lys Ser Ile Gly Pro Thr Cys Pro Phe Ala Gly Ser Cys Glu Val
55 40 45 50 55
57 agc aag act cag agg cgc cac tgc cca gcc tgc agg ttg cag aag tgc 485
58 Ser Lys Thr Gln Arg Arg His Cys Pro Ala Cys Arg Leu Gln Lys Cys
59 60 65 70
61 tta gat gct ggc atg agg aaa gac atg ata ctg tcg gca gaa gcc ctg 533

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62	Leu	Asp	Ala	Gly	Met	Arg	Lys	Asp	Met	Ile	Leu	Ser	Ala	Glu	Ala	Leu	
63			75						80					85			
65	gca	ttg	cgg	cga	gca	aag	cag	gcc	cag	cgg	cgg	gca	cag	caa	aca	cct	581
66	Ala	Leu	Arg	Arg	Ala	Lys	Gln	Ala	Gln	Arg	Arg	Ala	Gln	Gln	Thr	Pro	
67			90						95					100			
68	gtg	caa	ctg	agt	aag	gag	caa	gaa	gag	ctg	atc	cgg	aca	ctc	ctg	ggg	629
69	Val	Gln	Leu	Ser	Lys	Glu	Gln	Glu	Glu	Leu	Ile	Arg	Thr	Leu	Leu	Gly	
70			105						110					115			
73	gcc	cac	acc	cgc	cac	atg	ggc	acc	atg	ttt	gaa	cag	ttt	gtg	cag	ttt	677
74	Ala	His	Thr	Arg	His	Met	Gly	Thr	Met	Phe	Glu	Gln	Phe	Val	Gln	Phe	
75	120					125				130					135		
77	agg	cct	cca	gct	cat	ctg	ttc	atc	cat	cac	cag	ccc	ttg	ccc	acc	ctg	725
78	Arg	Pro	Pro	Ala	His	Leu	Phe	Ile	His	His	Gln	Pro	Leu	Pro	Thr	Leu	
79						140				145					150		
81	gcc	cct	gtg	ctg	cct	ctg	gtc	aca	cac	ttc	gca	gac	atc	aac	act	ttc	773
82	Ala	Pro	Val	Leu	Pro	Leu	Val	Thr	His	Phe	Ala	Asp	Ile	Asn	Thr	Phe	
83			155						160					165			
85	atg	gta	ctg	caa	gtc	atc	aag	ttt	act	aag	gac	ctg	ccc	gtc	ttc	cgt	821
86	Met	Val	Leu	Gln	Val	Ile	Lys	Phe	Thr	Lys	Asp	Leu	Pro	Val	Phe	Arg	
87			170						175					180			
89	tcc	ctg	ccc	att	gaa	gac	cag	atc	tcc	ctt	ctc	aag	gga	gca	gct	gtg	869
90	Ser	Leu	Pro	Ile	Glu	Asp	Gln	Ile	Ser	Leu	Leu	Lys	Gly	Ala	Ala	Val	
91			185						190					195			
93	gaa	atc	tgt	cac	atc	gta	ctc	aat	acc	act	ttc	tgt	ctc	caa	aca	caa	917
94	Glu	Ile	Cys	His	Ile	Val	Leu	Asn	Thr	Thr	Phe	Cys	Leu	Gln	Thr	Gln	
95	200					205				210					215		
97	aac	ttc	ctc	tgc	ggg	cct	ctt	cgc	tac	aca	att	gaa	gat	gga	gcc	cgt	965
98	Asn	Phe	Leu	Cys	Gly	Pro	Leu	Arg	Tyr	Thr	Ile	Glu	Asp	Gly	Ala	Arg	
99						220				225					230		
101	gtg	ggg	ttc	cag	gta	gag	ttt	ttg	gag	ttg	ctc	ttt	cac	ttc	cat	gga	1013
102	Val	Gly	Phe	Gln	Val	Glu	Phe	Leu	Glu	Leu	Leu	Phe	His	Phe	His	Gly	
103			235						240					245			
105	aca	cta	cga	aaa	ctg	cag	ctc	caa	gag	cct	gag	tat	gtg	ctc	ttg	gtc	1061
106	Thr	Leu	Arg	Lys	Leu	Gln	Leu	Gln	Glu	Pro	Glu	Tyr	Val	Leu	Leu	Ala	
107			250						255					260			
109	gcc	atg	gcc	ctc	ttc	tct	cct	gac	cga	cct	gga	gtt	acc	cag	aga	gat	1109
110	Ala	Met	Ala	Leu	Phe	Ser	Pro	Asp	Arg	Pro	Gly	Val	Thr	Gln	Arg	Asp	
111			265						270					275			
113	gag	att	gat	cag	ctg	caa	gag	gag	atg	gca	ctg	act	ctg	caa	agc	tac	1157
114	Glu	Ile	Asp	Gln	Leu	Gln	Glu	Glu	Met	Ala	Leu	Thr	Leu	Gln	Ser	Tyr	
115	280					285				290					295		
117	atc	aag	ggc	cag	cag	cga	agg	ccc	cg	gat	cg	ttt	ctg	tat	g	cg	1205
118	Ile	Lys	Gly	Gln	Gln	Arg	Arg	Pro	Arg	Asp	Arg	Phe	Leu	Tyr	Ala	Lys	
119						300				305					310		
121	ttg	cta	ggc	ctg	ctg	gct	gag	ctc	cg	agc	att	aat	gag	gcc	tac	gg	1253
122	Leu	Leu	Gly	Leu	Leu	Ala	Glu	Leu	Arg	Ser	Ile	Asn	Glu	Ala	Tyr	Gly	
123			315						320					325			
125	tac	caa	atc	cag	cac	atc	cag	ggc	ctg	tct	gcc	atg	atg	ccg	ctg	ctc	1301
126	Tyr	Gln	Ile	Gln	His	Ile	Gln	Gly	Leu	Ser	Ala	Met	Met	Pro	Leu	Leu	

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127	330	335	340	
129	cag gag atc tgc agc tgaggccatg ctcacttcct tccccagctc acctggaaca			1356
130	Gln Glu Ile Cys Ser			
131	345			
133	ccctggatac actggagtgg gaaaatgctg ggaccaaaga ttgggcccggg ttcaaaggga			1416
135	gcccagtggt tgcaatgaaa gactaaagca aaac			1450
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142	<211> LENGTH: 348			
143	<212> TYPE: PRT			
144	<213> ORGANISM: Homo sapiens			
146	<400> SEQUENCE: 2			
148	Met Ala Ser Arg Glu Asp Glu Leu Arg Asn Cys Val Val Cys Gly Asp			
149	1 5 10 15			
151	Gln Ala Thr Gly Tyr His Phe Asn Ala Leu Thr Cys Glu Gly Cys Lys			
152	20 25 30			
154	Gly Phe Phe Arg Arg Thr Val Ser Lys Ser Ile Gly Pro Thr Cys Pro			
155	35 40 45			
157	Phe Ala Gly Ser Cys Glu Val Ser Lys Thr Gln Arg Arg His Cys Pro			
158	50 55 60			
160	Ala Cys Arg Leu Gln Lys Cys Leu Asp Ala Gly Met Arg Lys Asp Met			
161	65 70 75 80			
163	Ile Leu Ser Ala Glu Ala Leu Ala Leu Arg Arg Ala Lys Gln Ala Gln			
164	85 90 95			
166	Arg Arg Ala Gln Gln Thr Pro Val Gln Leu Ser Lys Glu Gln Glu Glu			
167	100 105 110			
169	Leu Ile Arg Thr Leu Leu Gly Ala His Thr Arg His Met Gly Thr Met			
170	115 120 125			
172	Phe Glu Gln Phe Val Gln Phe Arg Pro Pro Ala His Leu Phe Ile His			
173	130 135 140			
175	His Gln Pro Leu Pro Thr Leu Ala Pro Val Leu Pro Leu Val Thr His			
176	145 150 155 160			
178	Phe Ala Asp Ile Asn Thr Phe Met Val Leu Gln Val Ile Lys Phe Thr			
179	165 170 175			
181	Lys Asp Leu Pro Val Phe Arg Ser Leu Pro Ile Glu Asp Gln Ile Ser			
182	180 185 190			
184	Leu Leu Lys Gly Ala Ala Val Glu Ile Cys His Ile Val Leu Asn Thr			
185	195 200 205			
187	Thr Phe Cys Leu Gln Thr Gln Asn Phe Leu Cys Gly Pro Leu Arg Tyr			
188	210 215 220			
190	Thr Ile Glu Asp Gly Ala Arg Val Gly Phe Gln Val Glu Phe Leu Glu			
191	225 230 235 240			
194	Leu Leu Phe His Phe His Gly Thr Leu Arg Lys Leu Gln Leu Gln Glu			
195	245 250 255			
197	Pro Glu Tyr Val Leu Leu Ala Ala Met Ala Leu Phe Ser Pro Asp Arg			
198	260 265 270			
200	Pro Gly Val Thr Gln Arg Asp Glu Ile Asp Gln Leu Gln Glu Glu Met			
201	275 280 285			
203	Ala Leu Thr Leu Gln Ser Tyr Ile Lys Gly Gln Gln Arg Arg Pro Arg			
204	290 295 300			

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206 Asp Arg Phe Leu Tyr Ala Lys Leu Leu Gly Leu Leu Ala Glu Leu Arg  
207 305 310 315 320  
209 Ser Ile Asn Glu Ala Tyr Gly Tyr Gln Ile Gln His Ile Gln Gly Leu  
210 325 330 335  
212 Ser Ala Met Met Pro Leu Leu Gln Glu Ile Cys Ser  
213 340 345  
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216 <211> LENGTH: 714  
217 <212> TYPE: DNA  
218 <213> ORGANISM: Homo sapiens  
220 <220> FEATURE:  
221 <221> NAME/KEY: CDS  
222 <222> LOCATION: (1)..(714)  
224 <400> SEQUENCE: 3  
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226 Pro Val Gln Leu Ser Lys Glu Gln Glu Glu Leu Ile Arg Thr Leu Leu  
227 1 5 10 15  
229 ggg gcc cac acc cgc cac atg ggc acc atg ttt gaa cag ttt gtg cag 96  
230 Gly Ala His Thr Arg His Met Gly Thr Met Phe Glu Gln Phe Val Gln  
231 20 25 30  
233 ttt agg cct cca gct cat ctg ttc atc cat cac cag ccc ttg ccc acc 144  
234 Phe Arg Pro Pro Ala His Leu Phe Ile His His Gln Pro Leu Pro Thr  
235 35 40 45  
237 ctg gcc cct gtg cct ctg gtc aca cac ttc gca gac atc aac act 192  
238 Leu Ala Pro Val Leu Pro Leu Val Thr His Phe Ala Asp Ile Asn Thr  
239 50 55 60  
241 ttc atg gta ctg caa gtc atc aag ttt act aag gac ctg ccc gtc ttc 240  
242 Phe Met Val Leu Gln Val Ile Lys Phe Thr Lys Asp Leu Pro Val Phe  
243 65 70 75 80  
245 cgt tcc ctg ccc att gaa gac cag atc tcc ctt ctc aag gga gca gct 288  
246 Arg Ser Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu Lys Gly Ala Ala  
247 85 90 95  
249 gtg gaa atc tgt cac atc gta ctc aat acc act ttc tgt ctc caa aca 336  
250 Val Glu Ile Cys His Ile Val Leu Asn Thr Thr Phe Cys Leu Gln Thr  
251 100 105 110  
253 caa aac ttc ctc tgc ggg cct ctt cgc tac aca att gaa gat gga gcc 384  
254 Gln Asn Phe Leu Cys Gly Pro Leu Arg Tyr Thr Ile Glu Asp Gly Ala  
255 115 120 125  
257 cgt gtg ggg ttc cag gta gag ttt ttg gag ttg ctc ttt cac ttc cat 432  
258 Arg Val Gly Phe Gln Val Glu Phe Leu Glu Leu Phe His Phe His  
259 130 135 140  
261 gga aca cta cga aaa ctg cag ctc caa gag cct gag tat gtg ctc ttg 480  
262 Gly Thr Leu Arg Lys Leu Gln Leu Gln Glu Pro Glu Tyr Val Leu Leu  
263 145 150 155 160  
265 gct gcc atg gcc ctc ttc tct cct gac cga cct gga gtt acc cag aga 528  
266 Ala Ala Met Ala Leu Phe Ser Pro Asp Arg Pro Gly Val Thr Gln Arg  
267 165 170 175  
269 gat gag att gat cag ctg caa gag gag atg gca ctg act ctg caa agc 576  
270 Asp Glu Ile Asp Gln Leu Gln Glu Met Ala Leu Thr Leu Gln Ser

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271               180               185               190  
 273 tac atc aag ggc cag cag cga agg ccc cgg gat cgg ttt ctg tat gcg       624  
 274 Tyr Ile Lys Gly Gln Gln Arg Arg Pro Arg Asp Arg Phe Leu Tyr Ala  
 275               195               200               205  
 277 aag ttg cta ggc ctg ctg gct gag ctc cgg agc att aat gag gcc tac       672  
 278 Lys Leu Leu Gly Leu Leu Ala Glu Leu Arg Ser Ile Asn Glu Ala Tyr  
 279               210               215               220  
 281 ggg tac caa atc cag cac atc cag ggc ctg tct gcc atg atg       714  
 282 Gly Tyr Gln Ile Gln His Ile Gln Gly Leu Ser Ala Met Met  
 283 225               230               235  
 285 <210> SEQ ID NO: 4  
 286 <211> LENGTH: 238  
 287 <212> TYPE: PRT  
 288 <213> ORGANISM: Homo sapiens  
 290 <400> SEQUENCE: 4  
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 293 1               5               10               15  
 295 Gly Ala His Thr Arg His Met Gly Thr Met Phe Glu Gln Phe Val Gln  
 296               20               25               30  
 298 Phe Arg Pro Pro Ala His Leu Phe Ile His His Gln Pro Leu Pro Thr  
 299               35               40               45  
 301 Leu Ala Pro Val Leu Pro Leu Val Thr His Phe Ala Asp Ile Asn Thr  
 302               50               55               60  
 304 Phe Met Val Leu Gln Val Ile Lys Phe Thr Lys Asp Leu Pro Val Phe  
 305 65               70               75               80  
 307 Arg Ser Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu Lys Gly Ala Ala  
 308               85               90               95  
 310 Val Glu Ile Cys His Ile Val Leu Asn Thr Thr Phe Cys Leu Gln Thr  
 311               100               105               110  
 313 Gln Asn Phe Leu Cys Gly Pro Leu Arg Tyr Thr Ile Glu Asp Gly Ala  
 314               115               120               125  
 316 Arg Val Gly Phe Gln Val Glu Phe Leu Glu Leu Leu Phe His Phe His  
 317               130               135               140  
 319 Gly Thr Leu Arg Lys Leu Gln Leu Gln Glu Pro Glu Tyr Val Leu Leu  
 320 145               150               155               160  
 322 Ala Ala Met Ala Leu Phe Ser Pro Asp Arg Pro Gly Val Thr Gln Arg  
 323               165               170               175  
 325 Asp Glu Ile Asp Gln Leu Gln Glu Glu Met Ala Leu Thr Leu Gln Ser  
 326               180               185               190  
 328 Tyr Ile Lys Gly Gln Gln Arg Arg Pro Arg Asp Arg Phe Leu Tyr Ala  
 329               195               200               205  
 331 Lys Leu Leu Gly Leu Leu Ala Glu Leu Arg Ser Ile Asn Glu Ala Tyr  
 332               210               215               220  
 334 Gly Tyr Gln Ile Gln His Ile Gln Gly Leu Ser Ala Met Met  
 335 225               230               235  
 338 <210> SEQ ID NO: 5  
 339 <211> LENGTH: 11  
 340 <212> TYPE: PRT  
 341 <213> ORGANISM: Artificial

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/27/2006  
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### Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#: 5, 6, 7

**VERIFICATION SUMMARY**

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L:16 M:270 C: Current Application Number differs, Replaced Current Application No

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date